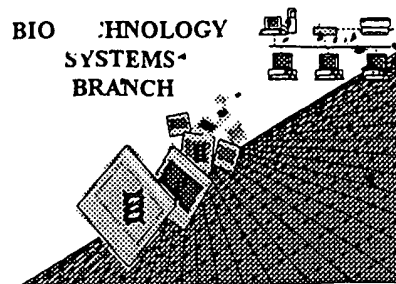


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/015078
Source: OIP E
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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

TIME: 09:39:29

Input Set : A:\235673-1.app

Output Set: N:\CRF3\09102001\I015078.raw

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Suerbaum, Sebastian
7 Labigne, Agnes

9 (ii) TITLE OF INVENTION: Cloning and Characterization of the flbA
10 Gene of H. Pylori, Production of Aflagellate Strains

12 (iii) NUMBER OF SEQUENCES: 13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
16 Dunner

17 (B) STREET: 1300 I Street, N.W.

18 (C) CITY: Washington

19 (D) STATE: D.C.

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3315

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/015,078

C--> 31 (B) FILING DATE: 23-Aug-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Meyers, Kenneth J.

36 (B) REGISTRATION NUMBER: 25,146

37 (C) REFERENCE/DOCKET NUMBER: 02356.0073-01000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (202) 408-4000

41 (B) TELEFAX: (202) 408-4400

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 19 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 ATGCCNGGNA AAGCARATG

61 (2) INFORMATION FOR SEQ ID NO: 2:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 18 base pairs

65 (B) TYPE: nucleic acid

66 (C) STRANDEDNESS: single

67 (D) TOPOLOGY: linear

69 (ii) MOLECULE TYPE: DNA (genomic)

Errored: Sequence listing must
conform to the Rules on the
CFR as of July 1, 1998.

Must use new format; Contact
Robert Wax at
703 306 4119

19

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

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Input Set : A:\235673-1.app

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74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
76 RAAATTTCATN GCNCCRTC                                     18
78 (2) INFORMATION FOR SEQ ID NO: 3:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 135 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: single
84          (D) TOPOLOGY: linear
86      (ii) MOLECULE TYPE: DNA (genomic)
91      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
93 ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTAAATT CAGGGCTTAT TGATGATAAG      60
95 GAAGCTAAAA AACGGCGCGC CGCTCTAAGC CAAGAAGCGG ATTTTATATG TGCGATGGAT      120
97 GCGCGCTCTA AATTT                                     135
99 (2) INFORMATION FOR SEQ ID NO: 4:
101      (i) SEQUENCE CHARACTERISTICS:
102          (A) LENGTH: 28 base pairs
103          (B) TYPE: nucleic acid
104          (C) STRANDEDNESS: single
105          (D) TOPOLOGY: linear
107      (ii) MOLECULE TYPE: DNA (genomic)
112      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
114 CGGGATCCGT GGTACTAAT GGTCTTAC                                     28
116 (2) INFORMATION FOR SEQ ID NO: 5:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 28 base pairs
120          (B) TYPE: nucleic acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
124      (ii) MOLECULE TYPE: DNA (genomic)
129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
131 CGGGATCCTC ATGGCCTCTT CAGAGACC                                     28
133 (2) INFORMATION FOR SEQ ID NO: 6:
135      (i) SEQUENCE CHARACTERISTICS:
136          (A) LENGTH: 2501 base pairs
137          (B) TYPE: nucleic acid
138          (C) STRANDEDNESS: single
139          (D) TOPOLOGY: linear
141      (ii) MOLECULE TYPE: DNA (genomic)
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
148 AGCTTTTTTG TGCCATACTT TTAACTTTA TATTATAATA AGAGACAAAC ACACCTACCA      60
150 AAATTAAGGC ATTGATTTTA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG      120
152 ACTTTCCTTG TCTTTAAACG CTTCTTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTTGTG      180
154 ATAGCGATTT TAGCGATCAT TATCGTGCCG TTACCGCCTT TTGTGTTGGA TTTTCTACTC      240
156 ACGATTTCTA TCGCGCTATC GGTGTTGATT ATTTTAATCG GGCTTTATAT TGACAAACCG      300
158 ACTGATTTTA GCGCTTTCCC CACTTTATTA CTCATTGTAA CCTTATACCG CTTGGCTTTA      360
160 AATGTCGCCA CCACTAGAAT GATTTTAACC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC      420
162 ATTATTATCA CGGCGTTTGG GGAATTTAGC GTGAGCGGGA ATTATGTGAT TGGGGCTATT      480
164 ATCTTTAGTA TTTTAGTGCT GGTGAATTTA TTAGTGTTTA CTAATGGTTC TACTAGGGTT      540
166 ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT      600

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RAW SEQUENCE LISTING

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168 GCGGATTTAA ATTGAGGGCT TATTGATGAT AAGGAAGCTA AAAAACGGCG CGCCGCTCTA      660
170 AGCCAAGAAG CGGATTTTTTA TGGTGCATG GATGGCGCGT CTAAATTTGT CAAAGGCGAT      720
172 GCGATCGCTT CTATCATTAT CACGCTTATC AATATCATTG GGGGTTTTTT AGTGGGCGTG      780
174 TTCCAAAGGG ATATGAGCTT GAGCTTTAGT GCTAGCACTT TCACTATCTT AACCATTGGC      840
176 GATGGGCTTG TAGGGCAAAT CCCTGCCTTA ATCATTGCGA CACGGACCGG TATTGTCGCC      900
178 ACTCGCACCA CGCAAAACGA AGAAGAGGAC TTTGCTTCTA AGCTCATCAC ACAGCTCACC      960
180 AATAAAAGCA AAACTTTAGT GATTGTGGGG GCGATTTATT GCTTTTGCAC CATTCTTGGA     1020
182 CTCCCTACCT TTTCTTTAGG GTTGTAGGG GCTCTCTTTT TATTCATCGC ATGCTGATT      1080
184 AGCAGGGAGG GAAAGGACGG GTTGCTCACT AAATTAGAAA ATTATTTGAG TCAAAAAATTC     1140
186 GGCTTGGAAT TGAGCGAAAA ACCCCACAGC TCCAAAATCA AACCCACGC CCCCACCACA     1200
188 AGGGCTAAAA CCCAAGAAGA GATTAAAAGA GAAGAAGAGC AAGCCATTGA TGAAGTGTTA     1260
190 AAAATTGAAT TTTTAGAATT GGCTTTAGGC TATCAGCTCT ACAGCTTAGC GGACATGAAA     1320
192 CAAGGGGGCG ATTTGTTAGA AAGGATTAGG GGTATTAGAA AAAAGATAGC GAGCGATTAT     1380
194 GGTTTTTTGA TGCCTCAAAT TAGGATTAGG GATAATTTAC AACTCCCCCC AACGCATTAT     1440
196 GAAATCAAGC TTAAGGGCAT TGTGATTGGT GAAGGCATGG TGATGCCGGA TAAGTTTTTA     1500
198 GCCATGAATA CCGGTTTTGT GAATAAAGAA ATTGAAGGCA TTCCTACTAA AGAGCCGGCT     1560
200 TTTGGAATGG ACGCTTTATG GATTGAAACT AAAAATAAAG AAGAAGCCAT CATTCAAGGC     1620
202 TATACCATTA TTGATCCAAG CACCGTTATT GCGACGCACA CCAGCGAATT AGTGAAAAAA     1680
204 TACGCTGAAG ATTTTATCAC TAAAGATGAA GTGAAATCCC TTTTAGAGCG CTTGGCCAAA     1740
206 GACTATCCTA CGATTGTAGA AGAGAGTAAA AAAATCCCCA CCGGTGCGAT CCGATCAGTC     1800
208 TTGCAAGCCT TGTGCGATGA AAAAATCCCC ATTAAAGACA TGCTCACTAT TTTAGAAACG     1860
210 ATTACCGATA TTGCGCCATT AGTTCAAAAC GATGTGAATA TCTTAACCGA ACAAGTGAGG     1920
212 GCGAGGCTTT CTAGGGTGAT CACTAACGCT TTTAAATCTG AAGACGGGCG TTTGAAATTT     1980
214 TTAACCTTTT CTACCGATAG CGAACAATTT TTGCTTAATA AATTGCGAGA AAATGGCACT     2040
216 TCTAAGAGCC TACTACTCAA TGTGGGCGAA TTGCAAAAAC TCATTGAAGC GGTCTCTGAA     2100
218 GAGGCCATGA AAGTCTTGCA AAAAGGGATC GCTCCGGTGA TTTTGATCGT AGAGCCTAAT     2160
220 TTAAGAAAAG CCCTTTCTAA TCAAATGGAG CAGGCTAGGA TTGATGTAAT CGTGCTAAGC     2220
222 CATGCTGAAT TAGATCCTAA CTCTAATTTT GAAGCCTTAG GCACGATCCA TATTAACTTT     2280
224 TAAGGGATAA ATAATTGATA AAAAAGGAGA ATGATGCAAG TTTATCACCT TTCACACATT     2340
226 GATTTAGACG GCTATGCATG CCAGCTTGTT TCAAAACAAT TTTTAAAAAA TATCCAATGC     2400
228 TATAACGCTA ATTACGGGCG TGAAGTCTCA GCGAGAATTT ATGAGATTTT AAACGCGATC     2460
230 GCTCAATCTA AAGAGAGTGA ATTCCTTATT TTGATTAGCG A
232 (2) INFORMATION FOR SEQ ID NO: 7:
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 732 amino acids
235 (B) TYPE: amino acid
236 (C) STRANDEDNESS: single
237 (D) TOPOLOGY: linear
238 (ii) MOLECULE TYPE: peptide
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
240 Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
241 1 5 10 15
242 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
243 20 25 30
244 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
245 35 40 45
246 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu
247 50 55 60
248 Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr

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Output Set: N:\CRF3\09102001\I015078.raw

260	65	70	75	80
262	Leu Leu Leu Ile Val Thr Leu Tyr Arg Leu Ala Leu Asn Val Ala Thr			
263		85	90	95
265	Thr Arg Met Ile Leu Thr Gln Gly Tyr Lys Gly Pro Ser Ala Val Ser			
266		100	105	110
268	Ile Ile Ile Thr Ala Phe Gly Glu Phe Ser Val Ser Gly Asn Tyr Val			
269		115	120	125
271	Ile Gly Ala Ile Ile Phe Ser Ile Leu Val Leu Val Asn Leu Leu Val			
272		130	135	140
274	Val Thr Asn Gly Ser Thr Arg Val Thr Glu Val Arg Ala Arg Phe Ala			
275	145	150	155	160
277	Leu Asp Ala Met Pro Gly Lys Gln Met Ala Ile Asp Ala Asp Leu Asn			
278		165	170	175
280	Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu			
281		180	185	190
283	Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe			
284		195	200	205
286	Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile			
287		210	215	220
289	Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser			
290	225	230	235	240
292	Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Ala Gly Leu Val			
293		245	250	255
295	Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala			
296		260	265	270
298	Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile			
299		275	280	285
301	Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile			
302		290	295	300
304	Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe			
305	305	310	315	320
307	Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly			
308		325	330	335
310	Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe			
311		340	345	350
313	Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His			
314		355	360	365
316	Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu			
317		370	375	380
319	Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala			
320	385	390	395	400
322	Leu Gly Thr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp			
323		405	410	415
325	Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr			
326		420	425	430
328	Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro			
329		435	440	445
331	Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly			
332		450	455	460

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

TIME: 09:39:29

Input Set : A:\235673-1.app

Output Set: N:\CRF3\09102001\I015078.raw

```

334 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
335 465 470 475 480
337 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
338 485 490 495
340 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
341 500 505 510
343 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
344 515 520 525
346 Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
347 530 535 540
349 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
350 545 550 555 560
352 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
353 565 570 575
355 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
356 580 585 590
358 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
359 595 600 605
361 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
362 610 615 620
364 Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
365 625 630 635 640
367 Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
368 645 650 655
370 Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
371 660 665 670
373 Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
374 675 680 685
376 Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
377 690 695 700
379 Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
380 705 710 715 720
382 Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
383 725 730
385 (2) INFORMATION FOR SEQ ID NO: 8:
387 (i) SEQUENCE CHARACTERISTICS:
388 (A) LENGTH: 732 amino acids
389 (B) TYPE: amino acid
390 (C) STRANDEDNESS: single
391 (D) TOPOLOGY: linear
393 (ii) MOLECULE TYPE: peptide
398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
400 Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
401 1 5 10 15
403 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
404 20 25 30
406 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
407 35 40 45
409 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

TIME: 09:39:30

Input Set : A:\235673-1.app

Output Set: N:\CRF3\09102001\I015078.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]